



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Tripp, Cynthia A.  
Frank, Glenn R.  
Grieve, Robert B.

(ii) TITLE OF INVENTION: NOVEL PARASITIC HELMINTH  
P22U PROTEINS

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Sheridan Ross P.C.  
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(C) CITY: Denver  
(D) STATE: CO  
(E) COUNTRY: U.S.A.  
(F) ZIP: 80203

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/460,428  
(B) FILING DATE: 02-JUN-1995  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Connell, Gary J.  
(B) REGISTRATION NUMBER: 32,020  
(C) REFERENCE/DOCKET NUMBER: 2618-13-3

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 303/863-9700  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 913 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 3..911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GC GAG TTA AAT AGT CGA ATT TCC GGA GTA CAC CGT AAT ACT GCA GGT

Glu	Leu	Asn	Ser	Arg	Ile	Ser	Gly	Val	His	Arg	Asn	Thr	Ala	Gly	
1									10						15
GCT TTA CAA CGA TTT GCT CTA AAT GGT CAA AAT ACT CTT AAC GAA GGA														95	
Ala	Leu	Gln	Arg	Phe	Ala	Leu	Asn	Gly	Gln	Asn	Thr	Leu	Asn	Glu	Gly
									25						30
TCA AGT TAT GAG CCA AAC GGA CTA TTT GTA TTT TCA GCA ATA AAC GGT														143	
Ser	Ser	Tyr	Glu	Pro	Asn	Gly	Leu	Phe	Val	Phe	Ser	Ala	Ile	Asn	Gly
									40						45
AGC CAT ACT GAT AGC TTA TCT CAG TAT GGT GAA GGA ATA AAT GAA AAT														191	
Ser	His	Thr	Asp	Ser	Leu	Ser	Gln	Tyr	Gly	Glu	Gly	Ile	Asn	Glu	Asn
									55						60
TAT CAT TCT GGA ACT AAT TAT TAT GAT GAA GTA GAA TTA AGA GAT AAA														239	
Tyr	His	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Glu	Val	Glu	Leu	Arg	Asp	Lys
									70						75
ACA AAT CAG ACA TCG TAC ATT AAT GGA AAT GAT AAT GGA ATC AAT GGA														287	
Thr	Asn	Gln	Thr	Ser	Tyr	Ile	Asn	Gly	Asn	Asp	Asn	Gly	Ile	Asn	Gly
									80						95
AAG GAT GAT GAA GAT CTG GAT GAA TGC TCT GAT CAA GAA TTC CGA TGT														335	
Lys	Asp	Asp	Glu	Asp	Leu	Asp	Glu	Cys	Ser	Asp	Gln	Glu	Phe	Arg	Cys
									100						110
CCA TAT CTA GCT AAA ACA CTT TGT GTT CAT TAT TTG AAA ATA TGC GAT														383	
Pro	Tyr	Leu	Ala	Lys	Thr	Leu	Cys	Val	His	Tyr	Leu	Lys	Ile	Cys	Asp
									115						125
GGT ATT GAT GAT TGT GGT GAT GGA AGT GAT GAA ATG AAC TGT GCT GAT														431	
Gly	Ile	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Met	Asn	Cys	Ala	Asp
									130						140
GAT GAA GTG ATA ACA TCA ATA AAT GGT AAC GAA TCA ATC AAT ATC AGA														479	
Asp	Glu	Val	Ile	Thr	Ser	Ile	Asn	Gly	Asn	Glu	Ser	Ile	Asn	Ile	Arg
									145						155
TGT GAT CCG GAT CAA TTT CGA TGT GAA AAT GGA AAA TGT ATC GCA CAA														527	
Cys	Asp	Pro	Asp	Gln	Phe	Arg	Cys	Glu	Asn	Gly	Lys	Cys	Ile	Ala	Gln
									160						175
ATT GAT CGA TGT AAT CGA AAA TAT GAT TGT GAT GAT GGT ACA GAT GAA														575	
Ile	Asp	Arg	Cys	Asn	Arg	Lys	Tyr	Asp	Cys	Asp	Asp	Gly	Thr	Asp	Glu
									180						190
ACA ACT TGT GAA TAT TTC GTG CAA GCT TTG CAA CAA GCG AGA GGT GTA														623	
Thr	Thr	Cys	Glu	Tyr	Phe	Val	Gln	Ala	Leu	Gln	Gln	Ala	Arg	Gly	Val
									195						205
ACG GTG CAG GAT AAT GCA ATT CGA GAT GAC GAG ATA CCA AAT TAT ACT														671	
Thr	Val	Gln	Asp	Asn	Ala	Ile	Arg	Asp	Asp	Glu	Ile	Pro	Asn	Tyr	Thr
									210						220
GTA TCC ATG GAA CAG AAA TAC GAT CAA GTA AAG GAA GAT AAG GAG CGG														719	
Val	Ser	Met	Glu	Gln	Lys	Tyr	Asp	Gln	Val	Lys	Glu	Asp	Lys	Glu	Arg
									225						235
CGA ATG CAA GAG GAG GAG GAA CAG GAA AGG CTG AGA GAG TAC GAG GAA														767	
Arg	Met	Gln	Glu	Glu	Gln	Glu	Arg	Leu	Arg	Glu	Tyr	Glu	Glu		

240	245	250	255	
CAG ATA CAG GAA AAA TTG AGG CAG GAG GAA GAA AGA GAA CGG CAA GAA				815
Gln Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu				
260	265	270		
CAG GAA AGA AGA CAA AAG GAA CGA GAA AGA ATG GAA CAA GAA AGG ATA				863
Gln Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile				
275	280	285		
AGA CAA GAA TAT GAT GAA AAG GAA AGA CAA AGG CAA TAT GCT GAA CAG				911
Arg Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln				
290	295	300		
GC				913

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 303 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu	Leu	Asn	Ser	Arg	Ile	Ser	Gly	Val	His	Arg	Asn	Thr	Ala	Gly	Ala
1					5				10						15
Leu	Gln	Arg	Phe	Ala	Leu	Asn	Gly	Gln	Asn	Thr	Leu	Asn	Glu	Gly	Ser
					20			25							30
Ser	Tyr	Glu	Pro	Asn	Gly	Leu	Phe	Val	Phe	Ser	Ala	Ile	Asn	Gly	Ser
					35			40							45
His	Thr	Asp	Ser	Leu	Ser	Gln	Tyr	Gly	Glu	Gly	Ile	Asn	Glu	Asn	Tyr
					50			55			60				
His	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Glu	Val	Glu	Leu	Arg	Asp	Lys	Thr
					65			70			75				80
Asn	Gln	Thr	Ser	Tyr	Ile	Asn	Gly	Asn	Asp	Asn	Gly	Ile	Asn	Gly	Lys
					85			90							95
Asp	Asp	Glu	Asp	Leu	Asp	Glu	Cys	Ser	Asp	Gln	Glu	Phe	Arg	Cys	Pro
					100			105							110
Tyr	Leu	Ala	Lys	Thr	Leu	Cys	Val	His	Tyr	Leu	Lys	Ile	Cys	Asp	Gly
					115			120							125
Ile	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Met	Asn	Cys	Ala	Asp	Asp
					130			135			140				
Glu	Val	Ile	Thr	Ser	Ile	Asn	Gly	Asn	Glu	Ser	Ile	Asn	Ile	Arg	Cys
					145			150			155				160
Asp	Pro	Asp	Gln	Phe	Arg	Cys	Glu	Asn	Gly	Lys	Cys	Ile	Ala	Gln	Ile
					165			170							175

Asp Arg Cys Asn Arg Lys Tyr Asp Cys Asp Asp Gly Thr Asp Glu Thr  
 180 185 190  
 Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val Thr  
 195 200 205  
 Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr Val  
 210 215 220  
 Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg Arg  
 225 230 235 240  
 Met Gln Glu Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu Gln  
 245 250 255  
 Ile Gln Glu Lys Leu Arg Gln Glu Glu Arg Glu Arg Gln Glu Gln  
 260 265 270  
 Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile Arg  
 275 280 285  
 Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln  
 290 295 300

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..626

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 627..1016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GT TTT GTT GTA CTA CTC GTT GCA ATA TGG ATT GAA ATG AGC CAA	47
Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln	
1 5 10 15	
GGC CAA CAA ATG ATC AAA CAA TGT AAA TGT TCT GAT ATT GCA CCA TGT	95
Gly Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys	
20 25 30	
CAA TTA ACT GCC GTT CAA TCA GTT TTA CCA TGT GCT GAT CAA TGC CAG	143
Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln	
35 40 45	
AAA TAT ATT ACT TCA ATT GGT GGT AAT TAT GAT CAA ATT AGT AAC TGT	191
Lys Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys	
50 55 60	

TTT AAA CAG AAA CAA TCA ATT ATA AAT GAT GCT ATG AAA TGT GCT CAA Phe Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln 65 70 75	239
GAT GCT TTC CCA AAT GCA TGC GCA CAA GGT GAA CCA AAA ATG GTA CCA Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro 80 85 90 95	287
AAA CGA TTC GGA AAA GGT CTT CAA TTA GCT GTA ATG ACT GAT ATC AAC Lys Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn 100 105 110	335
AAA GAA TTA CAA CGA ATG GGA ATA GCA AAT CAA GTT ACT CAA CTA ATC Lys Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile 115 120 125	383
TCC CAA GGT CGA CGA TTC TTT AAA TGC TTC CAA TCG TGT ATG ATG AAA Ser Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys 130 135 140	431
AAA TTG GGC TCA TGT TCT CCA GAT TGT GGT CTT GAT TTA CCA TCT GAT Lys Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp 145 150 155	479
AAT GTT ATG GTT CAA ACA GTT AAA AAT TGC GCT CAA AAA AGT GGT ATT Asn Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile 160 165 170 175	527
CAA ACT GCA TCG GTG CAA GAT CTT TGC TTT TGC GTC GAA CAA GCT GGT Gln Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly 180 185 190	575
ATT CGG CAA CTT TCT GAT GTA TGT CCT CGT ATA CAA ATT TTC AAA ACG Ile Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr 195 200 205	623
AAA TGAGTATTGA GAATATTGCA CTAGCAGCAA TCATTATTT TCTCGAGAAT Lys	676
TTTCGCTATC AATAAGTTGG AATATGATTA CAATAATATA TATATTAAC T GCAAAATCT	736
TTCTTCTTCA AAATTATTTT TCATTTGCT CTCATAATTG CATGATAATA GTCATAATGA	796
AAAACAGGTT TTCTTTTTT AAAATGATAA CTTCAAACAA ATAGGTATTT CTTGATATAT	856
ATATGTATGT ATGTATGTGT GTGTGTGTGT GTGTGTGTAT GTGTGTGTT GTGTATGTGT	916
ATATGTATGT ATGTATGTAT GTATGTATGT ATGTGTAGGA GAAAAGCAAA CTAACAGTA	976
AATGAAAGAA AAAATAAGT CAAATAAAAG TTTGATAATT	1016

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 208 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln Gly  
1 5 10 15

Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys Gln  
20 25 30

Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln Lys  
35 40 45

Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys Phe  
50 55 60

Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln Asp  
65 70 75 80

Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro Lys  
85 90 95

Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn Lys  
100 105 110

Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile Ser  
115 120 125

Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys Lys  
130 135 140

Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp Asn  
145 150 155 160

Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile Gln  
165 170 175

Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly Ile  
180 185 190

Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr Lys  
195 200 205

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Asp Cys Gly Asp Gly Ser Asp Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Gln Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Ile Ala Pro Cys Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys  
1 5 10 15

Ala Asp Gln Cys Gln Lys  
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp Asn  
1 5 10 15

Val Met Val Gln Asp Val  
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCCG AGTTAAATAG TCG

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCAGGATCC TGCACCG

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAGAGAGA GAGAGAGAGA ACTAGTCTCG AGTTTTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..17  
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGYTCNCCNG AYTGYGG

17

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..17  
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGYAGTCCNG AYTGYGG

17

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..17  
(D) OTHER INFORMATION: /label= PROBE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGNACCATNA CRTTRTC

17

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..27  
(D) OTHER INFORMATION: /label= PROBE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGTTTGAAC CATAACATTA CAGATGG

27

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..25  
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTGCAATAT GGGATCCAAT GAGCC

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..25  
(D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCTAGTGCA GGATCCTCAA TACTC

25